

Title:

Association of RSV-A ON1 genotype with Increased Pediatric
Acute Lower Respiratory Tract Infection in Vietnam

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Figure legend

Supplementary Figure 1. Phylogenetic analysis of RSV subgroup A G-protein 2nd hypervariable region circulating in Khanh Hoa province during January 2010 - December 2012

Supplementary Figure 2. Phylogenetic analysis of RSV subgroup B G-protein 2nd hypervariable region circulating in Khanh Hoa province during January 2010 - December 2012

Phylogenetic analysis was executed by the Neighbor-Joining method with bootstrap test of 1000 replicates using MEGA ver. 5.2.2 software. Bootstrap values higher than 70 were considered to be statistically significant and indicated at each branch node. Scale bar represents evolutionary distance calculated using the Maximum Composite Likelihood method. The length of scale bar corresponds to number of nucleotide substitutions per site from the closest branching node. Distinct colored circles were used as indicator for ARI samples originated from different sampling years (2010, 2011 or 2012): GREEN-filled circles were used for ARI samples obtained during Jan 2010 - Dec 2010, BLUE-filled circles for ARI samples during Jan 2011 - Dec 2011 and RED-filled circles for ARI samples during Jan 2012 - Dec 2012. "ARI-" is followed by four digits sample specific ID number. We intentionally excluded some ARI samples with identical nucleotide sequences particularly from same sampling year.

Supplementary Tables

Supplementary Table 1. Multivariate log-binomial regression analysis of clinical severity comparison between RSV and Non-RSV pediatric ARI cases

In the log-binomial regression analysis, RSV-positive ARI cases (n=426) and Non-RSV ARI cases (n=1428) detected during January 2010 - December 2012 were included. Non-RSV ARI cases (n=1428) were used as the reference group. In the multivariate analysis, demographic variables, including sex, age, antibiotic usage prior to hospitalization, daycare attendance, co-infection with other respiratory viruses and underlying medical condition were adjusted for estimating adjusted Relative Risk (Adj RR) and 95% Confidence Interval (CI).

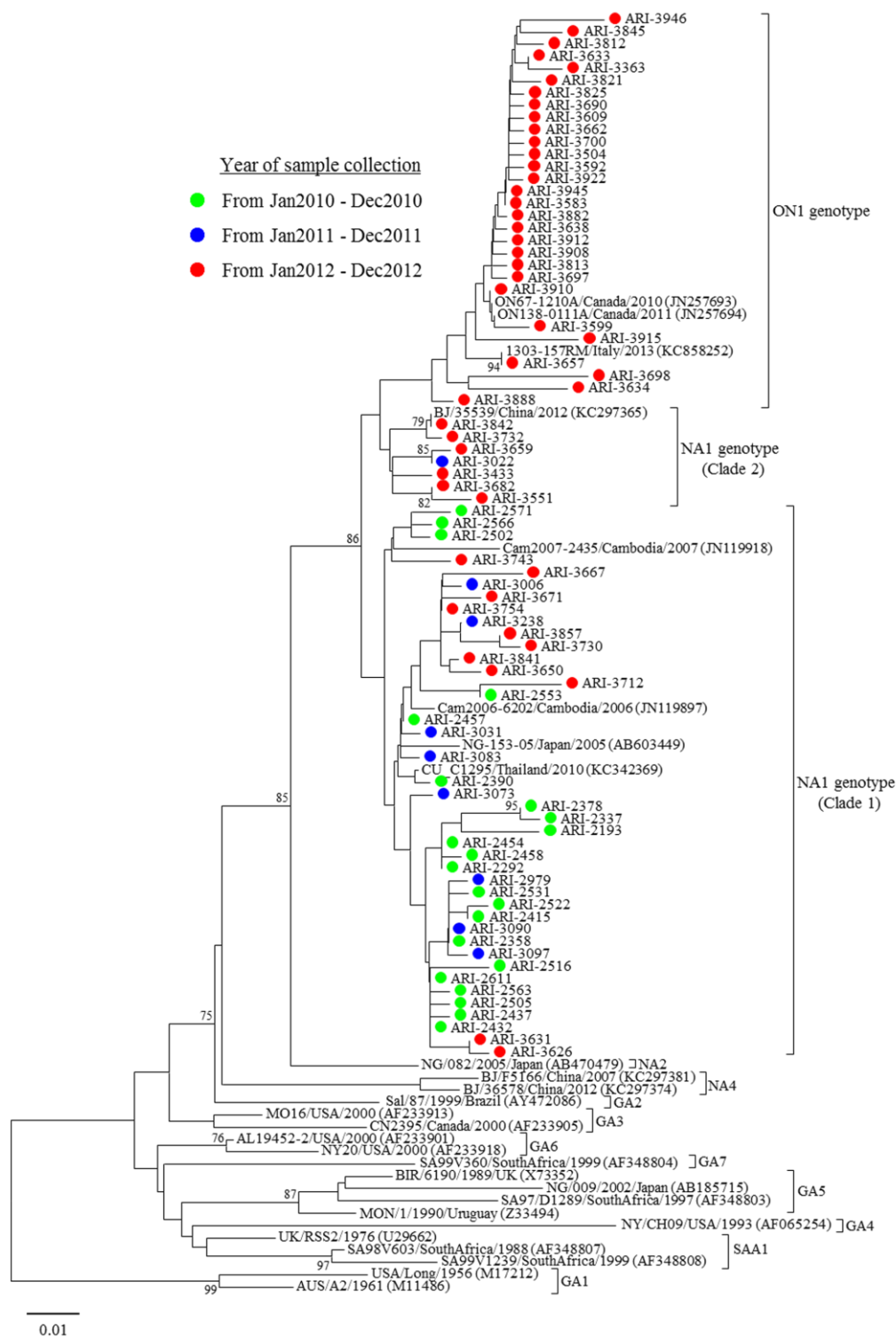


Fig. S1

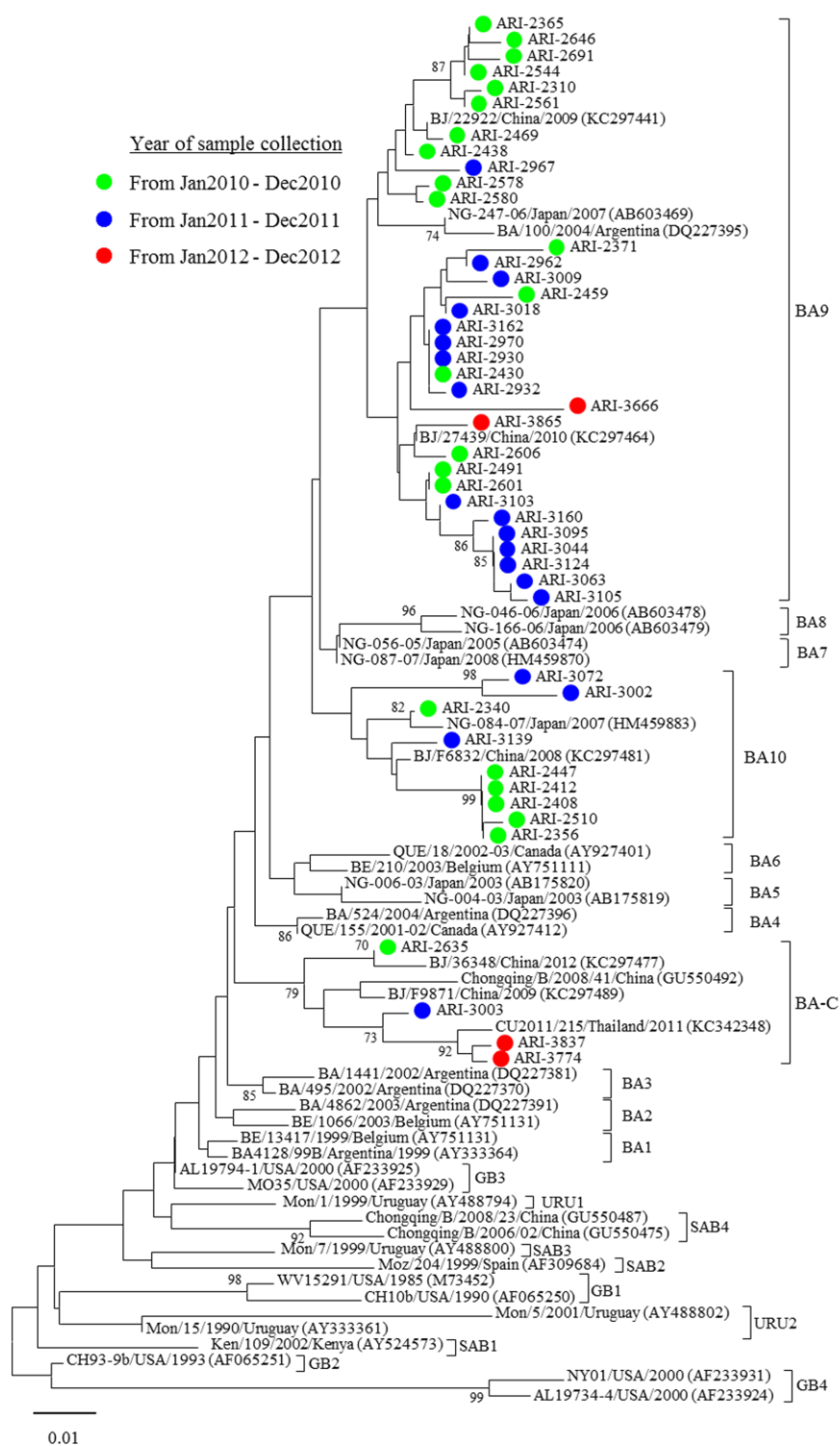


Fig. S2

Supplementary Table 1. Multivariate log-binomial regression analysis of clinical severity comparison between RSV and Non-RSV pediatric ARI cases

Clinical manifestation (s)	RSV / Non-RSV ARI cases	Unadjusted RR	95% CI [¶]	Adjusted RR [†]	95% CI [¶]
<u>Clinical symptom and sign (s)</u>					
Wheeze	RSV positive ARI cases (n=426)	1.15	1.04-1.28	1.16	1.03-1.30
	Non-RSV ARI cases (n=1428) [#]	(ref.)
Tachypnea		1.47	1.24-1.75	1.51	1.24-1.83
		
Crackle		1.32	1.07-1.64	1.48	1.19-1.85
		
Chest wall indrawing		1.45	1.03-2.05	1.60	1.05-2.44
		

[#] In the log-binomial regression analysis, Non-RSV ARI cases (n=1428) was used as the reference group.

[¶] 95%CI is abbreviation for 95% Confidence Interval.

[†] In the multivariate analysis using log-binomial regression, variables including sex, age, antibiotic use prior to hospitalization, daycare attendance, viral co-infection and underlying medical condition were adjusted for estimating adjusted Relative Risk (Adj RR) and 95% confidence Interval (CI).

All the statistically significant values were indicated in bold.